

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 21:34:47 ; Search time 80 Seconds
(without alignments)
65.907 Million cell updates/sec

Title: US-10-821-283-11

Perfect score: 58

Sequence: 1 QRILQQLNLPRI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21.*
1: Genesecp1980s.*
2: Genesecp1990s.*
3: Genesecp2000s.*
4: Genesecp2001s.*
5: Genesecp2002s.*
6: Genesecp2003as.*
7: Genesecp2003bs.*
8: Genesecp2004s.*
9: Genesecp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	12	6	ABR423328
2	55	94.8	12	6	ABR423338
3	55	94.8	12	6	ABR423339
4	50	86.2	12	6	ABR423337
5	49	84.5	10	6	ABR423341
6	48	82.8	10	6	ABR423340
7	43	74.1	628	7	ADH86368
8	39	67.2	410	7	ADH86368
9	39	67.2	498	6	ABU23712
10	38	65.5	158	4	AAU68928
11	38	65.5	158	7	ADH13248
12	38	65.5	158	8	ADH178457
13	38	65.5	169	8	ADY08869
14	38	65.5	248	9	ADV21130
15	38	65.5	500	8	ADSA4237
16	38	65.5	548	8	ADP43684
17	38	65.5	548	8	ABM83869
18	38	65.5	619	7	ADJ95176
19	38	65.5	619	7	ADK51032
20	38	65.5	623	7	ADK51028
21	38	65.5	635	8	ADQ39192
22	38	65.5	637	8	ADJ56820
23	38	65.5	638	5	ABG76951
24	38	65.5	638	7	ADJ95174
					Novel NOV

25	38	65.5	638	7	ADJ95172	Novel NOV
26	38	65.5	638	7	ADK51026	Human NOV
27	38	65.5	638	7	ADK51030	Human NOV
28	38	65.5	638	8	ADO39204	Human NOV
29	38	65.5	638	8	ADQ39191	Human myo
30	38	65.5	638	9	AEC00348	Human kal
31	37	63.8	13	4	AAU25227	Schizophr
32	37	63.8	13	4	AAU15571	Schizophr
33	37	63.8	13	8	ADO78838	Schizophr
34	37	63.8	89	6	ABM64994	Schizophr
35	37	63.8	91	4	AAU67514	Propionib
36	37	63.8	91	6	ABM64033	Propionib
37	37	63.8	171	4	ABE33448	Peptide #
38	37	63.8	171	4	AAU26908	Peptide #
39	37	63.8	171	4	ABE28269	Human pep
40	37	63.8	171	4	ABE18904	Protein #
41	37	63.8	171	4	ABG48295	Human liv
42	37	63.8	379	5	ABG96342	Human ova
43	37	63.8	386	8	ABM84109	Human dia
44	37	63.8	386	8	ABM84107	Human dia
45	37	63.8	386	8	ABM84105	Human dia
46	37	63.8	386	8	ABM84110	Human dia
47	37	63.8	387	1	AAU70502	Human pro
48	37	63.8	387	5	AAU78359	Modified
49	37	63.8	387	5	AAU78358	Modified
50	37	63.8	387	7	ADF72217	Human mut
51	37	63.8	387	7	ADF72207	Human mut
52	37	63.8	387	7	ADF72213	Human mut
53	37	63.8	387	7	ADF72215	Human mut
54	37	63.8	406	5	AAU78357	Human pro
55	37	63.8	406	7	ADF28937	Human pla
56	37	63.8	406	8	ADG20489	Human pro
57	37	63.8	406	8	ADR15124	Human pro
58	37	63.8	406	8	ADQ39551	Human myo
59	37	63.8	406	8	ADQ39548	Human myo
60	37	63.8	406	8	ADQ39549	Human myo
61	37	63.8	406	8	ADQ39552	Human myo
62	37	63.8	406	8	ADQ39550	Human myo
63	37	63.8	406	9	ADY62737	Human alp
64	37	63.8	416	8	ADR15126	Human pro
65	37	63.8	439	8	ADN17824	Bacterial
66	37	63.8	532	7	ABO64033	Klebsiell
67	37	63.8	1005	9	ADX39976	HIV Pol p
68	36	62.1	163	6	ADA55180	Human pro
69	36	62.1	337	4	AAU35653	Haemophil
70	36	62.1	337	6	ABU30607	Protein e
71	36	62.1	406	8	ADJ56053	Human fac
72	36	62.1	480	6	ABU29921	Protein e
73	36	62.1	501	6	ABU29921	Enterococ
74	36	62.1	501	6	ABU29375	Protein e
75	36	62.1	509	7	ADC95843	E. faeciu
76	36	62.1	513	7	ADH87242	Enterococ
77	36	62.1	714	7	ADJ70463	Human hea
78	36	62.1	729	8	ADH48379	Human KPP
79	36	62.1	1036	7	ABO78329	Human KPP
80	36	62.1	1112	8	ADS43238	Pseudomon
81	36	62.1	1115	4	AAU96812	Bacterial
82	36	62.1	1258	3	AAU80120	Putative
83	36	62.1	1258	4	AAU98987	Human Shi
84	36	62.1	1258	8	ADJ66611	Human typ
85	36	62.1	1258	8	ABM81289	Inositol
86	36	62.1	1302	8	ABE28331	Tumour-as
87	35	60.3	101	4	ABG04927	Human KPP
88	35	60.3	135	3	AAU94927	Novel hum
89	35	60.3	135	3	AAU94927	Novel hum
90	35	60.3	135	3	AAU94927	Novel hum
91	35	60.3	136	3	AAU94927	Novel hum
92	35	60.3	136	3	AAU94927	Novel hum
93	35	60.3	136	3	AAU94927	Novel hum
94	35	60.3	136	3	AAU94927	Novel hum
95	35	60.3	136	3	AAU94927	Novel hum
96	35	60.3	136	3	AAU94927	Novel hum
97	35	60.3	136	3	AAU94927	Novel hum

PT monoclonal antibodies, useful for treating cancer, autoimmune disease,
 PT inflammatory conditions or infections.

PS Claim 2; Page 5; 50pp; English.

XX The present sequence is that of a novel peptide comprising an epitope
 CC recognised by a BAT monoclonal antibody (MAB). It is a variant of peptide
 CC B (see ABR42328), which was isolated from a phage display random 12-mer
 CC peptide library, panning with BAT MAB. The peptide is capable of
 CC inhibiting the binding of BAT MAB to lymphoma cells, of inhibiting tumour
 CC growth, and of inducing an immune response against tumour cells. A
 CC claimed method for treating cancer comprises the administration of a
 CC pharmaceutical composition comprising e.g. the present peptide or a
 CC polynucleotide encoding it. A claimed immunomodulatory vaccine may also
 CC comprise the present peptide. The peptide can also be used as a
 CC diagnostic agent for detecting cancer, and to treat autoimmune disease,
 CC inflammatory conditions or infections

XX Sequence 10 AA;

Query Match 84.5%; Score 49; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QRILQINLP 10
 Db 1 QRILQINLP 10

RESULT 6

ABR42340
 ID ABR42340 standard; peptide; 10 AA.

XX ABR42340;

DT 11-AUG-2003 (first entry)

DE Immunomodulator peptide B variant.

XX Immunomodulator; immunotherapy; vaccine; monoclonal antibody; BAT;
 KW cytostatic; antiinflammatory.

XX Synthetic.

XX WO2003033644-A2.

XX 24-APR-2003.

XX 15-OCT-2002; 2002WO-IL000831.

XX 15-OCT-2001; 2001IL-00145926.

XX (CURE-) CURE TECH LTD.

PA (MORR-) MOR RES APPL LTD.

XX Hardy B, Raiter A, Klapper L;

XX WPI; 2003-421320/39.

DR N-PSDB; ACC57943.

XX New peptides comprising at least one epitope recognized by a BAT
 PT monoclonal antibodies, useful for treating cancer, autoimmune disease,
 PT inflammatory conditions or infections.

XX Claim 1; Page 5; 50pp; English.

XX The present sequence is that of a novel peptide comprising an epitope
 CC recognised by a BAT monoclonal antibody (MAB). It is a variant of peptide
 CC B (see ABR42328), which was isolated from a phage display random 12-mer
 CC peptide library, panning with BAT MAB. The peptide is capable of
 CC inhibiting the binding of BAT MAB to lymphoma cells, of inhibiting tumour
 CC growth, and of inducing an immune response against tumour cells. A
 CC claimed method for treating cancer comprises the administration of a

CC pharmaceutical composition comprising e.g. the present peptide or a
 CC polynucleotide encoding it. A claimed immunomodulatory vaccine may also
 CC comprise the present peptide. The peptide can also be used as a
 CC diagnostic agent for detecting cancer, and to treat autoimmune disease,
 CC inflammatory conditions or infections

XX Sequence 10 AA;

Query Match 82.8%; Score 48; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 ILQOINLPRI 12
 Db 1 ILQOINLPRI 10

RESULT 7

ABO83668

ID ABO83668 standard; protein; 628 AA.

XX ABO83668;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #15843.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD17239.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 32414; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX Sequence 628 AA;

XX Query Match 74.1%; Score 43; DB 7; Length 628;


```
QY      1 QRILQQLNLPRI 11
Db      201 ERILKLNLPRI 211
      :|||:::|:|
      :|||:::|:|

RESULT 10
ID AAU68928 standard; protein; 158 AA.
XX
AC AAU68928;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human protease domain of kallikrein 1.
XX
KW Human; Tumour associated differentially-expressed gene-12; TAGD-12;
KW cytosolic; ovarian cancer; transmembrane serine protease; LDLR-A domain;
KW SRCR domain protease domain; vaccine.
XX
OS Homo sapiens.
XX
PN US6294663-B1.
XX
PD 25-SEP-2001.
XX
PF 02-MAR-2000; 2000US-00518046.
XX
PR 03-MAR-1999; 99US-00261416.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Underwood LJ;
XX
DR WPI; 2001-647267/74.
XX
KW Tumour associated differentially expressed gene-12 and its encoded
PT protein, useful for detecting early and treating cancer, particularly
PT ovarian and other malignancies.
XX
PS Example 11; Fig 5C; 63pp; English.
XX
CC The invention relates to DNA encoding Tumour Associated Differentially
CC Expressed Gene-12 (TAGD-12) protein, a host cell containing the vector and
CC expressing the TAGD-12 protein, a host cell containing the vector and
CC antisense molecules directed against the nucleic acid. The TAGD-12
CC protein and DNA are useful for detecting early and treating cancer,
CC particularly ovarian and other malignancies(e.g by gene therapy). The
CC TAGD-12 protein (and peptides derived from it) is useful as a vaccine for
CC treating cancer. TAGD-12 is a transmembrane serine protease which
CC contains an LDLR-A (not defined) domain, an SRCR (not defined) domain and
CC a protease domain. The present sequence represents a domain from a
CC protein homologous to a domain from the TAGD-12 protein
XX
SQ Sequence 158 AA;
      Query Match 65.5%; Score 38; DB 4; Length 158;
      Best Local Similarity 50.0%; Pred. No. 97;
      Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 QRILQQLNLPRI 12
Db      106 QNLIKQVNIPLV 117
      :|||:::|:|
      :|||:::|:|

RESULT 11
ID ADE13248 standard; protein; 158 AA.
XX
AC ADE13248;
XX
DT 29-JAN-2004 (first entry)
XX
DE Protease domain from human kallikrein.
      Query Match 65.5%; Score 38; DB 7; Length 158;
      Best Local Similarity 50.0%; Pred. No. 97;
      Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

XX KW Human: Tumour Associated Differentially Expressed Gene-12; TAGD-12;
XX KW ovarian carcinoma; malignant hyperplasia; cancer; cytosolic;
XX KW transmembrane serine protease.
XX OS Homo sapiens.
XX PN US2003170707-A1.
XX PD 11-SEP-2003.
XX PF 03-FEB-2003; 2003US-00357175.
XX PR 02-MAR-2000; 2000US-00518046.
XX PR 28-AUG-2000; 2000US-00650371.
XX XX (OBRI/) O'BRIEN T J.
XX PI O'brien TJ;
XX DR WPI; 2003-863754/80.
XX PT A new DNA fragment encoding a Tumor Associated Differentially Expressed
XX Gene-12 (TAGD-12) protein which is a serine protease is useful to detect,
XX prevent and treat cancer, particularly lung, colon, prostate and ovarian
XX cancer.
XX PS Example 11; SEQ ID NO 22; 67pp; English.
XX CC The invention relates to a DNA fragment encoding a Tumour Associated
XX Differentially Expressed Gene-12 (TAGD-12) protein (a transmembrane
XX serine protease) or its splicing variants TAGD-12v and TAGD-12D (DNAs
XX appear as ADE13227, ADE13229 and ADE13370, the proteins as ADE13228,
XX ADE13230 and ADE13369). Also included are a vector comprising a TAGD-12
XX DNA and regulatory elements necessary for expressing the DNA in a cell, a
XX host cell transfected with the above vector and expressing a TAGD-12
XX protein, an antisense oligonucleotide complementary to TAGD-12 DNA, an
XX isolated and purified TAGD-12 protein encoded by TAGD-12 DNA, an antibody
XX directed against the TAGD-12 protein, detecting malignant hyperplasia
XX (comprising isolating mRNA from a sample and detecting mRNA encoding a
XX TAGD-12 protein or its variant where detected mRNA indicates malignant
XX hyperplasia), inhibiting expression of endogenous TAGD-12 mRNA in a cell
XX (comprising introducing into a cell a vector comprising a DNA fragment of
XX TAGD-12 in opposite orientation operably linked to elements necessary for
XX its expression), inhibiting expression of a TAGD-12 protein in a cell
XX (comprising introducing into the cell an antibody directed against TAGD-
XX 12 protein or its fragment), targeted therapy of an individual
XX (comprising administering a compound comprising a targeting moiety
XX specific for a TAGD-12 protein and a therapeutic moiety); vaccinating
XX against TAGD-12 (comprising inoculating with a TAGD-12 protein or its
XX fragment to elicit an immune response) and an immunogenic composition
XX comprising an immunogenic fragment of a TAGD-12 protein and an adjuvant.
XX The DNA, proteins, peptides and antibodies are used the diagnosis and
XX treatment of ovarian carcinoma, malignant hyperplasia and other cancers.
XX The present sequence represents a domain from a protein homologous to
XX TAGD-12.
XX SQ Sequence 158 AA;
      Query Match 65.5%; Score 38; DB 7; Length 158;
      Best Local Similarity 50.0%; Pred. No. 97;
      Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 QRILQQLNLPRI 12
Db      106 QNLIKQVNIPLV 117
      :|||:::|:|
      :|||:::|:|

RESULT 12
ADH78457
ID ADH78457 standard; protein; 158 AA.
XX
AC ADH78457;
```

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OM protein - protein search, using sw model

Run on: December 3, 2005, 21:35:02 ; Search time 15 Seconds
(without alignments)
76.973 Million cell updates/sec

Title: US-10-821-283-11
Perfect score: 58
Sequence: 1 QRILQINLPRI 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	343	2 P83126	ferric enterobacti
2	39	67.2	498	2 G97052	glycerol kinase, G
3	38	65.5	234	2 F42696	thrombin (EC 3.4.2
4	38	65.5	638	1 KOHUP	plasma kallikrein
5	37	63.8	334	2 A12150	serine/threonine k
6	37	63.8	370	2 T40131	hypothetical prote
7	37	63.8	406	2 A39339	protein C inhibito
8	37	63.8	1447	2 T22643	hypothetical prote
9	36	62.1	150	1 H69773	conserved hypothet
10	36	62.1	172	2 AC2548	hypothetical prote
11	36	62.1	235	2 D42696	thrombin (EC 3.4.2
12	36	62.1	236	2 I42696	thrombin (EC 3.4.2
13	36	62.1	316	1 A41171	3,4-dihydroxy-5-he
14	36	62.1	337	1 G64125	hematin transport pr
15	36	62.1	349	2 S54822	cbrC protein - Erw
16	36	62.1	942	2 G83038	probable sensor/re
17	36	62.1	1112	2 D75056	cell division cont
18	36	62.1	1258	2 JC5765	inositol polyphosp
19	36	62.1	2019	2 T27702	hypothetical prote
20	35	60.3	238	2 T12898	conserved hypothet
21	35	60.3	289	2 B65042	yfjp protein - Esc
22	35	60.3	327	2 S25071	hydroxymethylbilan
23	35	60.3	333	1 D69812	ferrichrome ABC tr
24	35	60.3	379	2 S63196	hypothetical prote
25	35	60.3	424	2 E95047	seryl-tRNA synthet
26	35	60.3	445	2 D97918	hemolysin secretio
27	35	60.3	583	2 S75805	probable exincucle
28	35	60.3	598	2 C71471	conserved hypothet
29	35	60.3	790	2 D83011	

30	35	60.3	998	2 T32787	hypothetical prote
31	35	60.3	1163	2 A56097	arylphorin-binding
32	35	60.3	1454	2 JC5144	muringlobulin pre
33	35	60.3	1536	2 S59841	4-alpha-glucanotra
34	35	60.3	2237	2 T21087	hypothetical prote
35	35	60.3	2245	2 T21086	hypothetical prote
36	34	58.6	149	2 A99088	hypothetical prote
37	34	58.6	149	2 P95223	hypothetical prote
38	34	58.6	207	2 A38143	protein kinase (EC
39	34	58.6	223	2 AE2224	two-component resp
40	34	58.6	235	2 H42696	thrombin (EC 3.4.2
41	34	58.6	268	2 B75279	survival protein S
42	34	58.6	307	2 AH1366	fructose-1-phospha
43	34	58.6	307	2 AH1366	fructose-1-phospha
44	34	58.6	323	2 AF2271	hypothetical prote
45	34	58.6	325	2 AC1333	conjugated bile ac
46	34	58.6	328	2 H83363	pyoverdine biosynt
47	34	58.6	338	2 S00085	protein kinase (EC
48	34	58.6	351	1 OKBO2C	protein kinase (EC
49	34	58.6	351	1 OKBOB1	protein kinase (EC
50	34	58.6	351	1 OKHU2C	protein kinase (EC
51	34	58.6	351	1 OKHUCB	protein kinase (EC
52	34	58.6	351	1 OKHYCA	protein kinase (EC
53	34	58.6	351	1 OKMSCA	protein kinase (EC
54	34	58.6	351	1 OKRT2C	protein kinase (EC
55	34	58.6	352	1 BEVECHD	molybdenum transpo
56	34	58.6	352	1 AE0595	ATP-binding compon
57	34	58.6	352	2 B85579	ATP-binding compon
58	34	58.6	352	2 A90728	ATP-binding compon
59	34	58.6	397	1 OKBOB2	protein kinase (EC
60	34	58.6	401	2 T02380	hypothetical prote
61	34	58.6	425	2 H97851	serine-tRNA ligase
62	34	58.6	470	2 S71466	homeotic protein S
63	34	58.6	585	2 JC6556	Y chromosome sex-d
64	34	58.6	595	2 JC6550	sex-determining re
65	34	58.6	641	2 D83046	selenocysteine-spe
66	34	58.6	660	2 B64243	lactococcin transp
67	34	58.6	660	2 S73597	lactococcin transp
68	34	58.6	683	2 S44780	C30A5.5 protein -
69	34	58.6	688	2 G83234	hypothetical prote
70	34	58.6	690	2 F71239	hypothetical prote
71	34	58.6	691	2 F82987	conserved hypothet
72	34	58.6	700	2 D90926	hypothetical prote
73	34	58.6	700	2 H85774	hypothetical prote
74	34	58.6	700	2 A64925	probable oxidoredu
75	34	58.6	745	1 OPHUM	myeloperoxidase (E
76	34	58.6	794	2 S59069	Z13 protein - mous
77	34	58.6	808	2 G83210	conserved hypothet
78	34	58.6	813	2 JC5785	ATP-dependent RNA
79	34	58.6	821	1 A39616	protein kinase RAD
80	34	58.6	825	2 C28894	myeloperoxidase (E
81	34	58.6	830	2 B28894	myeloperoxidase (E
82	34	58.6	844	2 S77547	ethylene response
83	34	58.6	1082	2 S64903	regulatory protein
84	34	58.6	1171	2 A42916	metabotropic gluta
85	34	58.6	1180	2 JC2132	metabotropic gluta
86	34	58.6	1212	2 JC2131	metabotropic gluta
87	34	58.6	1218	2 S71376	glutamate receptor
88	34	58.6	1250	1 B45219	N-methyl-D-asparta
89	34	58.6	1482	2 S13495	pregnancy zone pro
90	33	56.9	58	2 D82697	hypothetical prote
91	33	56.9	134	1 MWVZK5	K5 protein - vacci
92	33	56.9	136	2 D42505	K5L protein - vacc
93	33	56.9	178	2 A56836	hypothetical prote
94	33	56.9	184	2 S55435	hypothetical prote
95	33	56.9	206	2 S01049	hypothetical prote
96	33	56.9	208	2 B75359	endopeptidase-rela
97	33	56.9	236	2 C42696	thrombin (EC 3.4.2
98	33	56.9	239	2 G42696	thrombin (EC 3.4.2
99	33	56.9	288	2 E64750	ykfa protein - Esc
100	33	56.9	291	2 AH0049	probable transcrip

ALIGNMENTS

RESULT 1
F83126
ferric enterobactin transport protein PepG PA4161 [imported] - Pseudomonas aeruginosa (B
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83126
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bz
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83126
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <STO>
A:Cross-references: UNIPROT:Q9HWM0; UNIPARC:UPI00000C5C46; GB:AE004832; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pepG; PA4161

Query Match 74.1%; Score 43; DB 2; Length 343;
Best Local Similarity 58.3%; Pred. No. 2, 8;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR 12
:||||:|
Db 65 QRIVQVRLPRV 76

RESULT 2
G97062
glycerol kinase, GLPK [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97062
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G97062
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-498 <KUR>
A:Cross-references: UNIPROT:Q97JG4; UNIPARC:UPI000012B781; GB:AE001437; PIDN:AAK79290.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1321
C:Superfamily: xylulokinase

Query Match 67.2%; Score 39; DB 2; Length 498;
Best Local Similarity 54.5%; Pred. No. 24;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR 11
:||||:|
Db 201 ERILRLNLNIPR 211

RESULT 3
F42696
thrombin (EC 3.4.21.5) B chain - Cynops pyrogastor (fire-bellied newt) (fragment)
C:Species: Cynops pyrogastor (fire-bellied newt)
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: F42696
R:Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A:Reference number: A42696; MUID:92212913; PMID:1557383

A:Note: sequence not
A:Accession: F42696
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual t
A:Molecule type: mRNA
A:Residues: 1-234 <BAN>
A:Cross-references: UNIPROT:Q90387; UNIPARC:UPI0000175C59; GB:M81395
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: hydrolase; serine proteinase

Query Match 65.5%; Score 38; DB 2; Length 234;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RILQOINLPL 10
:||||:|
Db 133 QVLQOQNLPL 141

RESULT 4
KQHUP
plasma kallikrein (EC 3.4.21.34) precursor - human
N:Alternate names: kininogenin; plasma prekallikrein
C:Species: Homo sapiens (man)
C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 05-Oct-2004
C:Accession: A00921; A37939
R:Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A:Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four
A:Reference number: A00921; MUID:86243359; PMID:3521732
A:Accession: A00921
A:Molecule type: mRNA
A:Residues: 1-638 <CHU>
A:Cross-references: UNIPROT:P03952; UNIPARC:UPI000000DBAE; GB:M13143; NID:GI90262; PID:
R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A:Title: Location of the disulfide bonds in human plasma prekallikrein: the presence o
A:Reference number: A37939; MUID:91152016; PMID:1998666
A:Accession: A37939
A:Molecule type: protein
A:Residues: 20-27,40-46,'X',48,'H',50,'X',52-70,'H',75-76,'X',78-80,103-113,131-140,14
;260-283,'X',285;287-294,'X',293-295;314-317,'X',319-320;321-324,'X',329-333;334-339,'
525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 <MCM>
A:Cross-references: UNIPARC:UPI0000172B42; UNIPARC:UPI0000172B43; UNIPARC:UPI0000172B4
B49; UNIPARC:UPI0000172B4A; UNIPARC:UPI0000172B4B; UNIPARC:UPI0000172B4C; UNIPARC:UPI0
I0000172B52; UNIPARC:UPI0000172B53; UNIPARC:UPI0000172B54; UNIPARC:UPI0000172B55; UNIP
C:Comment: This protein, synthesized in the liver, circulates as a noncovalent complex
C:Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a
are linked by one or more disulfide bonds.
C:Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal
inogen and may also play a role in the renin-angiotensin system by converting prorenin
C:Genetics:
A:Gene: GDB:KLK3
A:Cross-references: GDB:127575; OMIM:229000
A:Map position: 4q35-q35
A:Superfamily: plasma kallikrein/coagulation factor XI; trypsin homology
C:Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inf
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-638/Product: plasma kallikrein #status predicted <MAT>
F:20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F:20-109/Domain: apple repeat <AP1>
F:110-199/Domain: apple repeat <AP2>
F:200-289/Domain: apple repeat <AP3>
F:291-380/Domain: apple repeat <AP4>
F:391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F:391-621/Domain: trypsin homology <TRY>
F:21-104,47-77;51-57;111-194,137-166;141-147;201-284,227-256;231-237,292-375,322-328,3
F:127,308,396,453,494/Binding site: carbohydrate (Aen) (covalent) #status experimental
F:318-347,340-345/Disulfide bonds: #status predicted
F:390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F:434,483,578/Active site: His, Asp, Ser #status predicted

Query Match 65.5%; Score 38; DB 1; Length 638;
Best Local Similarity 50.0%; Pred. No. 48;

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OM protein - protein search, using sw model

Run on: December 3, 2005, 21:39:47 ; Search time 73 Seconds
(without alignments)
115.977 Million cell updates/sec

Title: US-10-821-283-11
Perfect score: 58
Sequence: 1 QRI1QQINLPRI_12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	75.1	310	2	Q4KJ56_PSEF5
2	43	74.9	343	2	Q9HWM0_PSEAE
3	42	72.4	343	2	Q4KAK6_PSEF5
4	41	70.7	593	2	Q6SR34_MANSW
5	40	69.0	261	2	Q82254_CHLVC
6	40	69.0	355	2	Q5LNI3_SILPO
7	40	69.0	1134	2	Q71B05_BRARE
8	39	67.2	245	2	Q6D465_ERWCT
9	39	67.2	273	2	Q8L132_9CYAN
10	39	67.2	342	2	Q73TJ2_MYCPA
11	39	67.2	408	2	Q835G0_ENTFA
12	39	67.2	498	1	GLPK_CLOAB
13	39	67.2	647	2	Q639F7_BACCC
14	38	65.5	209	2	Q6HV36_BACAN
15	38	65.5	235	2	Q90387_CYNPY
16	38	65.5	381	2	Q636X3_BACCC
17	38	65.5	455	2	Q6BYK3_DEBHA
18	38	65.5	516	2	Q8BZ08_MOUSE
19	38	65.5	564	2	Q5R502_PONPY
20	38	65.5	609	2	Q7M761_MOUSE
21	38	65.5	638	1	KLKB1_HUMAN
22	38	65.5	638	2	Q4WSC3_HUMAN
23	38	65.5	643	2	Q97506_PIG
24	38	65.5	657	2	Q6CSX9_KLULA
25	38	65.5	700	2	Q5TSE1_ANOGA
26	38	65.5	790	2	Q4SS44_TETNG
27	37	63.8	47	2	Q7ZDB1_9HIVI
28	37	63.8	102	2	Q66070_9ALEP
29	37	63.8	212	2	Q5DYV6_VIBF1
30	37	63.8	227	2	Q6TBL8_9CHRO
31	37	63.8	227	2	Q6TBL9_MICAE

32	37	63.8	231	2	Q6BFN9_PARTE
33	37	63.8	295	2	Q8L145_9CHRO
34	37	63.8	305	2	Q99CY2_BHV4
35	37	63.8	326	2	Q6D2H9_ERWCT
36	37	63.8	334	2	Q8YTF7_ANASP
37	37	63.8	357	2	Q4R6X6_MACFA
38	37	63.8	365	2	Q88EK3_PSEPK
39	37	63.8	370	2	Q14341_9CHPO
40	37	63.8	378	2	Q90WP0_TRASC
41	37	63.8	382	2	Q90WT4_CRONI
42	37	63.8	385	2	Q90WS2_9SAUR
43	37	63.8	406	1	IPSP_HUMAN
44	37	63.8	406	2	Q4R6H4_MACFA
45	37	63.8	427	2	Q4FR92_9GAMM
46	37	63.8	431	2	Q57U90_9TRYP
47	37	63.8	554	2	Q6MEU8_PARUM
48	37	63.8	600	2	Q5R976_PONPY
49	37	63.8	967	1	RAPA_ERWCT
50	37	63.8	1005	2	Q8UTH8_9HIVI
51	37	63.8	1316	2	Q4TAP7_TETNG
52	37	63.8	1388	2	Q7ZWL0_XENLA
53	37	63.8	1405	2	Q4L1S8_GIBZE
54	37	63.8	1423	1	YAO6_CABEL
55	37	63.8	3779	2	Q55GD2_DICDI
56	36	62.1	96	2	Q84QZ4_ORYSA
57	36	62.1	128	2	Q84QZ1_ORYSA
58	36	62.1	130	2	Q4SKA7_TETNG
59	36	62.1	150	1	SPRL_BACSU
60	36	62.1	163	2	Q96WM0_HUMAN
61	36	62.1	169	2	Q8LBK6_ARATH
62	36	62.1	172	2	Q8ZS42_ANASP
63	36	62.1	209	2	Q4K5W6_PSEF5
64	36	62.1	209	2	Q8QO68_PSEPK
65	36	62.1	231	2	Q6LV70_PHOPR
66	36	62.1	240	2	Q6NJZ7_EDEBA
67	36	62.1	263	2	Q7NNM1_GLOVI
68	36	62.1	297	2	Q8PMN7_XANAC
69	36	62.1	316	1	COQ3_YEAST
70	36	62.1	322	2	Q5WSH6_LEGPL
71	36	62.1	322	2	Q5ZRB0_LEGPH
72	36	62.1	326	2	Q7R418_GIALA
73	36	62.1	327	2	Q6CUN1_KLULA
74	36	62.1	337	1	Y1471_HAEIN
75	36	62.1	349	1	CBRC_ERWCH
76	36	62.1	364	2	Q63F74_BACCC
77	36	62.1	420	2	Q90504_EPTST
78	36	62.1	426	1	SYS_FRATT
79	36	62.1	482	2	Q5P8C3_AZOSE
80	36	62.1	482	2	Q6N3X8_RHOPA
81	36	62.1	494	2	Q7PNM9_ANOGA
82	36	62.1	500	1	GLPK_ENTFA
83	36	62.1	560	2	Q4NTL2_9DELT
84	36	62.1	564	2	Q6CUK9_KLULA
85	36	62.1	567	2	Q95XW5_CABEL
86	36	62.1	607	2	Q91001_CHICK
87	36	62.1	748	2	Q74EZ7_GEOSL
88	36	62.1	760	2	Q5SRA9_MOUSE
89	36	62.1	768	2	Q7VBV4_PROMA
90	36	62.1	911	2	Q86H89_DICDI
91	36	62.1	942	2	Q9HUV7_PSAE
92	36	62.1	1112	2	Q9UYR7_PYRAB
93	36	62.1	1149	2	Q13577_HUMAN
94	36	62.1	1258	2	Q15357_HUMAN
95	36	62.1	3322	2	Q6BEQ3_CABEL
96	36	62.1	3323	2	Q6BEQ4_CABEL
97	36	62.1	3405	2	Q6BEQ5_CABEL
98	36	62.1	3436	2	Q86NF8_CABEL
99	36	62.1	3436	2	Q86NF9_CABEL
100	36	62.1	3436	2	Q18290_CABEL

ALIGNMENTS

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RESULT 1
Q4KJ56_PSEFS
ID Q4KJ56_PSEFS PRELIMINARY; PRT; 310 AA.
AC Q4KJ56;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PFL0585;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.,
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878 (2005).
RL EMBL; CP000076; AAY95992.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 310 AA; 3338 MW; B8DCA857C68C22B1 CRC64;

Query Match 75.9%; Score 44; DB 2; Length 310;
Best Local Similarity 75.0%; Pred. No. 8.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR1 12
Db 21 QRIESQINLPR1 32

RESULT 2
Q9HWM0_PSEAE
ID Q9HWM0_PSEAE PRELIMINARY; PRT; 343 AA.
AC Q9HWM0;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferric enterobactin transport protein fepG.
GN Name=fepG; OrderedLocusNames=PA4161;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
RL EMBL; AE004832; AAG07548.1; -; Genomic_DNA.
DR PIR; F83126; F83126.
DR HSP; P06609; L17V.
DR GO; GO:0014020; C:membrane; IEA.
DR GO; GO:0005293; F:lysine permease activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.

RESULT 3
Q4KAK6_PSEFS
ID Q4KAK6_PSEFS PRELIMINARY; PRT; 343 AA.
AC Q4KAK6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ferric vibriobactin ABC transporter, permease protein VC0778.
GN ORFNames=PFL3625;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.,
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878 (2005).
RL EMBL; CP000076; AAY92891.1; -; Genomic_DNA.
SQ SEQUENCE 343 AA; 35251 MW; 43943608CADE978C CRC64;

Query Match 72.4%; Score 42; DB 2; Length 343;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR1 11
Db 65 QRVLQVRLPR 75

RESULT 4
Q6SR94_MANSM
ID Q6SR94_MANSM PRELIMINARY; PRT; 593 AA.
AC Q6SR94;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MSI909;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281 (2004).

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OM protein - protein search, using sw model

Run on: December 3, 2005, 21:44:48 ; Search time 46 Seconds
(without alignments)
21.568 Million cell updates/sec

Title: US-10-821-283-11
Perfect score: 58
Sequence: 1 QRILQINLPRI 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	628	2	US-09-252-991A-32414
2	39	67.2	410	2	US-09-134-000C-4253
3	38	65.5	158	2	US-09-518-046-22
4	38	65.5	158	2	US-09-650-371-22
5	38	65.5	232	2	US-09-959-392-31
6	38	65.5	248	2	US-08-944-483-63
7	37	63.8	414	2	US-09-949-016-8143
8	37	63.8	532	2	US-09-489-039A-10550
9	36	62.1	207	2	US-09-248-796A-16787
10	36	62.1	509	2	US-09-107-532A-5470
11	36	62.1	513	2	US-09-134-000C-5127
12	36	62.1	1036	2	US-09-252-991A-27075
13	36	62.1	1149	2	US-08-560-005-5
14	36	62.1	1149	2	US-09-418-540-5
15	36	62.1	1149	2	US-09-969-528-5
16	36	62.1	1254	2	US-09-949-016-7777
17	36	62.1	1258	2	US-09-922-543-1
18	36	62.1	1258	2	US-10-742-430-1
19	35	60.3	137	2	US-08-844-065-4
20	35	60.3	251	2	US-09-489-039A-9846
21	35	60.3	344	2	US-09-134-001C-5567
22	35	60.3	374	2	US-09-583-110-392A
23	35	60.3	396	2	US-09-107-532A-7045
24	35	60.3	404	2	US-08-844-065-2
25	35	60.3	414	2	US-09-107-433-4985
26	35	60.3	424	1	US-08-920-634-2
27	35	60.3	466	2	US-09-270-767-60926

28	35	60.3	497	1	US-08-252-492-2	Sequence 2, Appli
29	35	60.3	497	1	US-08-727-126-2	Sequence 2, Appli
30	35	60.3	497	1	US-08-942-761-2	Sequence 2, Appli
31	35	60.3	515	2	US-09-543-681A-8280	Sequence 8280, Ap
32	35	60.3	549	2	US-09-270-767-45421	Sequence 45421, A
33	35	60.3	790	2	US-09-252-991A-33052	Sequence 33052, A
34	35	60.3	1002	2	US-10-290-579A-187	Sequence 187, App
35	34	58.6	124	2	US-09-513-999C-4892	Sequence 4892, Ap
36	34	58.6	140	2	US-09-771-161A-103	Sequence 103, App
37	34	58.6	144	2	US-09-394-455-43	Sequence 43, Appl
38	34	58.6	144	2	US-09-394-455-45	Sequence 45, Appl
39	34	58.6	149	2	US-09-583-110-3674	Sequence 3674, Ap
40	34	58.6	243	2	US-09-270-767-36305	Sequence 36305, A
41	34	58.6	243	2	US-09-270-767-51522	Sequence 51522, A
42	34	58.6	260	1	US-08-061-636-4	Sequence 4, Appli
43	34	58.6	260	1	US-07-857-224B-2	Sequence 2, Appli
44	34	58.6	260	1	US-07-857-224B-3	Sequence 3, Appli
45	34	58.6	260	1	US-07-857-224B-3	Sequence 4, Appli
46	34	58.6	260	4	PCT-US94-05268-4	Sequence 17527, A
47	34	58.6	295	2	US-09-248-796A-17527	Sequence 9455, Ap
48	34	58.6	327	2	US-09-949-016-9455	Sequence 2, Appli
49	34	58.6	336	2	US-09-394-455-2	Sequence 15, Appl
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51	34	58.6	343	2	US-09-394-455-34	Sequence 38, Appl
52	34	58.6	343	2	US-09-394-455-38	Sequence 37, Appl
53	34	58.6	350	2	US-09-457-040B-37	Sequence 946, App
54	34	58.6	350	2	US-09-538-092-946	Sequence 991, App
55	34	58.6	351	2	US-09-457-040B-6	Sequence 6, Appli
56	34	58.6	351	2	US-09-394-455-4	Sequence 4, Appli
57	34	58.6	351	2	US-09-771-161A-194	Sequence 194, App
58	34	58.6	352	2	US-09-711-164-448	Sequence 448, App
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60	34	58.6	412	2	US-09-252-991A-17935	Sequence 17935, A
61	34	58.6	436	2	US-09-252-991A-25475	Sequence 25475, A
62	34	58.6	505	2	US-10-104-047-3420	Sequence 3420, Ap
63	34	58.6	595	2	US-09-417-197-69	Sequence 69, Appl
64	34	58.6	622	2	US-09-949-016-6651	Sequence 6651, Ap
65	34	58.6	622	2	US-09-949-016-11128	Sequence 11128, A
66	34	58.6	725	2	US-09-252-991A-23752	Sequence 23752, A
67	34	58.6	738	2	US-09-252-991A-22930	Sequence 22930, A
68	34	58.6	761	2	US-09-949-016-9802	Sequence 9802, Ap
69	34	58.6	776	1	US-08-198-448B-17	Sequence 17, Appl
70	34	58.6	776	1	US-08-870-693-17	Sequence 17, Appl
71	34	58.6	788	2	US-09-248-796A-14753	Sequence 14753, A
72	34	58.6	821	1	US-08-198-446B-6	Sequence 6, Appli
73	34	58.6	821	1	US-08-870-693-6	Sequence 6, Appli
74	34	58.6	821	1	US-09-602-787A-578	Sequence 578, App
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76	34	58.6	877	1	US-08-486-270-12	Sequence 12, Appl
77	34	58.6	877	1	US-08-367-264-12	Sequence 12, Appl
78	34	58.6	877	2	US-09-153-757-12	Sequence 12, Appl
79	34	58.6	877	2	US-09-459-715-12	Sequence 12, Appl
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82	34	58.6	1043	2	US-09-538-092-533	Sequence 533, App
83	34	58.6	1082	2	US-09-252-991A-27256	Sequence 27256, A
84	34	58.6	1112	1	US-08-072-574-8	Sequence 8, Appli
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87	34	58.6	1180	2	US-08-660-148-2	Sequence 2, Appli
88	34	58.6	1180	2	US-09-153-757-8	Sequence 8, Appli
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90	34	58.6	1212	1	US-08-072-574-10	Sequence 10, Appl
91	34	58.6	1212	1	US-08-486-270-10	Sequence 10, Appl
92	34	58.6	1212	2	US-08-367-264-10	Sequence 10, Appl
93	34	58.6	1212	2	US-08-660-148-5	Sequence 5, Appli
94	34	58.6	1212	2	US-09-153-757-10	Sequence 10, Appl
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96	34	58.6	1212	2	US-09-695-481-7	Sequence 7, Appli
97	34	58.6	1212	2	US-10-037-417-110	Sequence 110, App
98	34	58.6	1429	2	US-10-037-417-36	Sequence 36, Appl
99	34	58.6	1479	2	US-09-471-276-1152	Sequence 1152, Ap
100	33	56.9	38	2		

ALIGNMENTS

RESULT 1
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; Sequence 32414, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32414
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32414

Query Match 74.1%; Score 43; DB 2; Length 628;
Best Local Similarity 58.3%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRILQQINLPRI 12
|||:|:|:
DB 350 QRIVORLPRV 361

RESULT 2
US-09-134-000C-4253
; Sequence 4253, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4253
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4253

Query Match 67.2%; Score 39; DB 2; Length 410;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RILQQINLPRI 12
|||:|:|:
DB 335 RIQKANLPKI 345

RESULT 3
US-09-518-046-22
; Sequence 22, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.

; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 22
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: protease domain of plasma kallikrein (Kal)
US-09-518-046-22

Query Match 65.5%; Score 38; DB 2; Length 158;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QRILQQINLPRI 12
|||:|:|:
DB 106 QNILQKNIPLV 117

RESULT 4
US-09-650-371-22
; Sequence 22, Application US/09650371
; Patent No. 6942978
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP/D
; CURRENT APPLICATION NUMBER: US/09/650,371
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/518,046
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 22
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: protease domain of plasma kallikrein (Kal)
US-09-650-371-22

Query Match 65.5%; Score 38; DB 2; Length 158;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QRILQQINLPRI 12
|||:|:|:
DB 106 QNILQKNIPLV 117

RESULT 5
US-09-959-392-31
; Sequence 31, Application US/09959392
; Patent No. 6806075
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL JOHN
; APPLICANT: WU, QINGYU
; APPLICANT: YAN, WEI
; TITLE OF INVENTION: CORIN, A SERINE PROTEASE
; FILE REFERENCE: BERLX 74A
; CURRENT APPLICATION NUMBER: US/09/959,392
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: PCT/EP99/03895
; PRIOR FILING DATE: 1999-06-04

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OM protein - protein search, using sw model

Run on: December 3, 2005, 21:47:24 ; Search time 163 Seconds
(without alignments)
30.760 Million cell updates/sec

Title: US-10-821-283-11
Perfect score: 58
Sequence: 1 OR10QINLPRI 12

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	49	84.5	10	5	US-10-821-283-16
6	48	82.8	10	5	US-10-821-283-15
7	39	67.2	498	4	US-10-821-283-15
8	38	65.5	136	4	US-10-821-283-15
9	38	65.5	158	4	US-10-357-175-22
10	38	65.5	158	4	US-10-455-720-22
11	38	65.5	169	4	US-10-425-114-64684
12	38	65.5	222	5	US-10-826-083-31
13	38	65.5	248	3	US-09-789-210-63
14	38	65.5	500	4	US-10-369-493-21167
15	38	65.5	619	4	US-10-403-161-52
16	38	65.5	619	4	US-10-287-226-404
17	38	65.5	621	4	US-10-403-161-48
18	38	65.5	635	4	US-10-741-601-304
19	38	65.5	635	5	US-10-741-600-855
20	38	65.5	638	3	US-09-808-602-102
21	38	65.5	638	3	US-09-800-198-85
22	38	65.5	638	4	US-10-099-198-85
23	38	65.5	638	4	US-10-099-322-111
24	38	65.5	638	4	US-10-099-322-112
25	38	65.5	638	4	US-10-044-564-30
26	38	65.5	638	4	US-10-044-564-111
27	38	65.5	638	4	US-10-044-564-112

28	65.5	638	4	US-10-403-161-46	Sequence 46, Appl
29	65.5	638	4	US-10-403-161-50	Sequence 50, Appl
30	65.5	638	4	US-10-287-226-400	Sequence 400, Appl
31	65.5	638	4	US-10-287-226-402	Sequence 402, Appl
32	65.5	638	4	US-10-287-226-658	Sequence 658, Appl
33	65.5	638	4	US-10-741-601-303	Sequence 303, Appl
34	65.5	638	5	US-10-741-600-854	Sequence 854, Appl
35	65.5	643	3	US-09-808-602-103	Sequence 103, Appl
36	65.5	643	3	US-09-800-198-86	Sequence 86, Appl
37	65.5	643	4	US-10-099-322-113	Sequence 113, Appl
38	65.5	643	4	US-10-044-564-113	Sequence 113, Appl
39	63.8	13	3	US-09-791-378-456	Sequence 456, Appl
40	63.8	13	3	US-09-791-377-456	Sequence 456, Appl
41	63.8	171	3	US-10-424-599-281910	Sequence 281910, A
42	63.8	171	3	US-09-864-761-34202	Sequence 34202, A
43	63.8	207	4	US-10-424-599-151363	Sequence 151363, A
44	63.8	379	4	US-10-097-340-139	Sequence 139, Appl
45	63.8	379	6	US-11-050-928-139	Sequence 139, Appl
46	63.8	406	5	US-10-741-600-1211	Sequence 1211, Appl
47	63.8	406	5	US-10-741-600-1212	Sequence 1212, Appl
48	63.8	406	5	US-10-741-600-1213	Sequence 1213, Appl
49	63.8	406	5	US-10-741-600-1214	Sequence 1214, Appl
50	63.8	406	5	US-10-741-600-1215	Sequence 1215, Appl
51	63.8	499	4	US-10-369-493-477	Sequence 477, Appl
52	62.1	47	4	US-10-425-115-279758	Sequence 279758, A
53	62.1	128	4	US-10-437-963-138160	Sequence 138160, A
54	62.1	163	4	US-10-094-749-2748	Sequence 2748, Appl
55	62.1	316	5	US-10-486-309-4	Sequence 4, Appl
56	62.1	334	4	US-10-437-963-186892	Sequence 186892, A
57	62.1	337	3	US-09-815-242-11246	Sequence 11246, A
58	62.1	337	4	US-10-282-122A-58531	Sequence 58531, A
59	62.1	480	4	US-10-282-122A-57845	Sequence 57845, A
60	62.1	501	3	US-09-815-242-10866	Sequence 10866, A
61	62.1	501	3	US-10-282-122A-57299	Sequence 57299, A
62	62.1	714	4	US-10-408-765A-3269	Sequence 3269, Appl
63	62.1	1112	4	US-10-369-493-21668	Sequence 21668, A
64	62.1	1149	3	US-09-969-528-5	Sequence 5, Appl
65	62.1	1258	3	US-09-922-543-1	Sequence 1, Appl
66	62.1	1258	4	US-10-742-431-1	Sequence 1, Appl
67	62.1	1258	4	US-10-742-430-1	Sequence 1, Appl
68	62.1	1258	5	US-10-742-071-1	Sequence 1, Appl
69	60.3	87	4	US-10-424-599-252704	Sequence 252704, A
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71	60.3	113	4	US-10-437-963-173306	Sequence 173306, A
72	60.3	122	4	US-10-424-599-273891	Sequence 273891, A
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74	60.3	164	5	US-10-889-890-6	Sequence 6, Appl
75	60.3	169	4	US-10-425-114-50302	Sequence 50302, A
76	60.3	226	4	US-10-425-114-41882	Sequence 41882, A
77	60.3	226	4	US-10-425-114-55235	Sequence 55235, A
78	60.3	244	4	US-10-425-115-251403	Sequence 251403, A
79	60.3	251	4	US-10-104-271-6	Sequence 6, Appl
80	60.3	287	4	US-10-282-122A-56029	Sequence 56029, A
81	60.3	289	4	US-10-282-122A-43225	Sequence 43225, A
82	60.3	293	5	US-10-450-763-59268	Sequence 59268, A
83	60.3	302	3	US-09-735-713A-4	Sequence 4, Appl
84	60.3	302	5	US-10-889-890-4	Sequence 4, Appl
85	60.3	306	4	US-10-104-271-13	Sequence 2, Appl
86	60.3	306	4	US-10-311-035-20	Sequence 13, Appl
87	60.3	306	5	US-10-487-462-4	Sequence 20, Appl
88	60.3	306	5	US-10-889-890-2	Sequence 4, Appl
89	60.3	327	4	US-10-369-493-1548	Sequence 1548, Appl
90	60.3	344	4	US-10-724-972A-7313	Sequence 7313, Appl
91	60.3	350	4	US-10-424-599-251218	Sequence 251218, A
92	60.3	414	5	US-10-617-320-4985	Sequence 4985, Appl
93	60.3	424	5	US-10-472-928-664	Sequence 664, Appl
94	60.3	424	5	US-10-953-901-491	Sequence 491, Appl
95	60.3	424	5	US-10-953-901-493	Sequence 493, Appl
96	60.3	445	4	US-10-282-122A-73799	Sequence 73799, A
97	60.3	476	4	US-10-425-115-23776	Sequence 23776, A
98	60.3	476	4	US-10-425-114-64608	Sequence 64608, A
99	60.3	477	4	US-10-425-114-64543	Sequence 64543, A
100	60.3	477	4	US-10-425-114-64543	Sequence 64543, A

ALIGNMENTS

RESULT 1

US-10-821-283-11
; Sequence 11, Application US/10821283
; Publication No. US20050003397A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/10/821,283
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal antibody
US-10-821-283-11

Query Match 100.0%; Score 58; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRILQQLNLPRI 12
Db 1 QRILQQLNLPRI 12

RESULT 2

US-10-821-283-13
; Sequence 13, Application US/10821283
; Publication No. US20050003397A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/10/821,283
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal antibody
US-10-821-283-13

Query Match 94.8%; Score 55; DB 5; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0042;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRILQQLNLPRI 12
Db 1 QRILQQLNLPRI 12

RESULT 3

US-10-821-283-14
; Sequence 14, Application US/10821283
; Publication No. US20050003397A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/10/821,283
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal antibody
US-10-821-283-14

Query Match 94.8%; Score 55; DB 5; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0042;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRILQQLNLPRI 12
Db 1 QRILQQLNLPRI 12

RESULT 4

US-10-821-283-12
; Sequence 12, Application US/10821283
; Publication No. US20050003397A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/10/821,283
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal antibody
US-10-821-283-12

Query Match 86.2%; Score 50; DB 5; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.034;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ORILQOINLPRI 12
|||||
Db 1 ORILQOINLARI 12
|||||

RESULT 5

US-10-821-283-16
; Sequence 16, Application US/10821283
; Publication No. US20050003397A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/10/821,283
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal antibody
US-10-821-283-16

Query Match 84.5%; Score 49; DB 5; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORILQOINLP 10
|||||
Db 1 ORILQOINLP 10
|||||

RESULT 6

US-10-821-283-15
; Sequence 15, Application US/10821283
; Publication No. US20050003397A1
; GENERAL INFORMATION:
; APPLICANT: CURE TECH LTD.
; APPLICANT: MOR-RESEARCH APPLICATIONS LTD.
; APPLICANT: HARDY, Britta
; APPLICANT: RAITER, Annat
; APPLICANT: KLAPPER, Leah
; TITLE OF INVENTION: PEPTIDES USEFUL IN IMMUNOMODULATION
; FILE REFERENCE: 85189-6100
; CURRENT APPLICATION NUMBER: US/10/821,283
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: PCT/IL02/00831
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: IL 145926
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant peptide recognized by the BAT-1 monoclonal antibody
US-10-821-283-15

Query Match 82.8%; Score 48; DB 5; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILQOINLPRI 12
|||||
Db 1 ILQOINLPRI 10
|||||

RESULT 7

US-10-282-122A-51636
; Sequence 51636, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangau
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51636
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51636

Query Match 67.2%; Score 39; DB 4; Length 498;

Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORILQOINLPRI 11
:||||:|
Db 201 ERILKUNIPR 211
:||||:|

RESULT 8

US-10-424-599-200575
; Sequence 200575, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 200575
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(136)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23144C.1.pep
US-10-424-599-200575

Query Match 65.5%; Score 38; DB 4; Length 136;
Best Local Similarity 70.0%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RILQOINLPR 11
| | | | |
Db 97 RILHHVNLPR 106

RESULT 9

US-10-357-175-22
; Sequence 22, Application US/10357175
; Publication No. US20030170707A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 22
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: protease domain of plasma kallikrein (Kal)
US-10-357-175-22

Query Match 65.5%; Score 38; DB 4; Length 158;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR 12
| | | | |
Db 106 QNIIQKVNIPLV 117

RESULT 10

US-10-455-720-22
; Sequence 22, Application US/10455720
; Publication No. US20030207316A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP/D2
; CURRENT APPLICATION NUMBER: US/10/455,720

; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 22
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: protease domain of plasma kallikrein (Kal)
US-10-455-720-22

Query Match 65.5%; Score 38; DB 4; Length 158;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR 12
| | | | |
Db 106 QNIIQKVNIPLV 117

RESULT 11

US-10-425-114-64684
; Sequence 64684, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64684
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4573-002-D11_FLI.pep
US-10-425-114-64684

Query Match 65.5%; Score 38; DB 4; Length 169;
Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRILQOINLPR 11
| | | | |
Db 119 QRLLEQLVLP 129

RESULT 12

US-10-926-083-31
; Sequence 31, Application US/10926083
; Publication No. US20050026255A1
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL JOHN
; APPLICANT: WU, QINGYU
; APPLICANT: YAN, WEI
; TITLE OF INVENTION: CORIN, A SERINE PROTEASE
; FILE REFERENCE: BERLX 74A
; CURRENT APPLICATION NUMBER: US/10/926,083
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: US/09/959,392
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: PCT/EP99/03895
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 09/092,029

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OM protein - protein search, using sw model

Run on: December 3, 2005, 21:48:44 ; Search time 11 Seconds
(without alignments)

5.224 Million cell updates/sec

Title: US-10-821-283-11

Perfect score: 58

Sequence: 1 QRILQINLPRI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA.New.*
1: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pap.*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pap.*
5: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pap.*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pap.*
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	62.1	1187	6	US-10-821-234-955
2	34	58.6	19	6	US-10-503-575-286
3	34	58.6	350	6	US-10-497-767-4
4	34	58.6	591	7	US-11-082-389-386
5	34	58.6	795	6	US-10-821-234-1675
6	34	58.6	870	7	US-11-082-389-384
7	33	56.9	19	6	US-10-503-575-285
8	33	56.9	892	7	US-11-082-389-396
9	32	55.2	225	6	US-10-793-626-1452
10	32	55.2	272	6	US-10-467-657-9017
11	32	55.2	288	6	US-10-793-626-1118
12	31.5	54.3	586	6	US-10-131-826A-46
13	31	53.4	29	6	US-10-467-657-2976
14	31	53.4	232	6	US-10-821-234-1023
15	31	53.4	554	6	US-10-793-626-1414
16	31	53.4	708	6	US-10-623-155-369
17	30	51.7	36	6	US-10-467-657-6822
18	30	51.7	157	6	US-10-793-626-2888
19	30	51.7	334	6	US-10-793-626-2972
20	30	51.7	334	6	US-10-467-657-2204
21	30	51.7	34	6	US-10-467-657-6504
22	30	51.7	481	6	US-10-467-657-3916
23	30	51.7	1076	6	US-10-467-657-7916
24	29	50.0	148	7	US-11-055-822-1076
25	29	50.0	155	6	US-10-467-657-7322
26	29	50.0	183	7	US-11-069-642-125
27	29	50.0	203	7	US-11-055-822-294
28	29	50.0	230	6	US-10-793-626-1054
29	29	50.0	232	7	US-11-055-822-628
30	29	50.0	432	7	US-11-055-822-292
31	29	50.0	473	6	US-10-467-657-298
32	29	50.0	473	6	US-10-467-657-298
33	29	50.0	473	6	US-10-467-657-298
34	29	50.0	733	7	US-11-012-762-68
35	29	50.0	792	6	US-10-793-626-1492
36	29	50.0	834	6	US-10-131-826A-148
37	29	50.0	841	6	US-10-624-932-6
38	29	50.0	841	6	US-10-624-932-8
39	28.5	49.1	1614	6	US-10-821-234-903
40	28	48.3	53	6	US-10-467-657-6084
41	28	48.3	156	6	US-10-467-657-546
42	28	48.3	195	7	US-10-508-263-106
43	28	48.3	207	6	US-11-038-284-26
44	28	48.3	240	7	US-10-467-657-8262
45	28	48.3	240	7	US-11-082-389-166
46	28	48.3	271	7	US-11-179-977-10
47	28	48.3	279	6	US-10-466-794A-3
48	28	48.3	290	6	US-10-131-826A-222
49	28	48.3	347	6	US-10-821-234-1081
50	28	48.3	376	7	US-11-082-383-122
51	28	48.3	376	6	US-11-082-389-124
52	28	48.3	377	6	US-10-467-657-680
53	28	48.3	377	6	US-10-467-657-4946
54	28	48.3	408	7	US-11-082-389-164
55	28	48.3	431	7	US-11-169-013-2
56	28	48.3	437	6	US-10-521-596-2
57	28	48.3	765	6	US-10-131-826A-28
58	28	48.3	1379	6	US-10-793-626-3188
59	28	48.3	1389	6	US-10-467-657-334
60	28	48.3	3056	7	US-11-109-156-20
61	28	48.3	5179	7	US-11-108-172-1068
62	27.5	47.4	854	7	US-11-022-562-219
63	27	46.6	75	6	US-10-821-234-1173
64	27	46.6	92	7	US-11-053-076-121
65	27	46.6	96	7	US-11-053-076-186
66	27	46.6	107	7	US-11-053-076-45
67	27	46.6	143	6	US-10-467-657-3812
68	27	46.6	147	6	US-10-793-626-2338
69	27	46.6	159	6	US-10-821-234-1321
70	27	46.6	165	6	US-10-467-657-702
71	27	46.6	176	6	US-10-793-626-362
72	27	46.6	189	6	US-10-793-626-2692
73	27	46.6	204	6	US-10-980-388-102
74	27	46.6	228	6	US-10-467-657-7522
75	27	46.6	249	6	US-10-467-657-4500
76	27	46.6	271	6	US-10-793-626-726
77	27	46.6	293	6	US-10-793-626-2646
78	27	46.6	338	6	US-10-793-626-2868
79	27	46.6	357	6	US-10-793-626-1936
80	27	46.6	481	6	US-10-467-657-4660
81	27	46.6	526	7	US-11-055-822-124
82	27	46.6	554	7	US-11-055-822-998
83	27	46.6	558	6	US-10-793-626-1760
84	27	46.6	582	7	US-11-074-176-110
85	27	46.6	729	7	US-11-099-691-3
86	27	46.6	732	6	US-10-467-657-5888
87	27	46.6	1009	6	US-10-467-657-186
88	27	46.6	1069	6	US-10-467-657-4556
89	27	46.6	1065	7	US-11-191-374-16
90	27	46.6	1065	7	US-11-191-374-16
91	27	46.6	1068	7	US-11-191-374-45
92	27	46.6	1068	7	US-11-191-374-17
93	27	46.6	1069	7	US-11-191-375-17
94	27	46.6	1210	7	US-11-108-172-692
95	27	46.6	1275	6	US-10-821-234-1598
96	27	46.6	1548	7	US-11-108-172-1095
97	27	46.6	1548	7	US-11-108-172-1095
98	27	46.6	3144	7	US-11-055-035-1

Sequence 7326, Ap
Sequence 125, App
Sequence 294, App
Sequence 1054, Ap
Sequence 628, App
Sequence 298, App
Sequence 6328, Ap
Sequence 68, Appl
Sequence 1492, Ap
Sequence 148, App
Sequence 6, Appli
Sequence 8, Appli
Sequence 9034, App
Sequence 6084, Ap
Sequence 546, App
Sequence 106, App
Sequence 26, Appl
Sequence 8262, Ap
Sequence 166, App
Sequence 10, Appl
Sequence 3, Appli
Sequence 222, App
Sequence 1081, Ap
Sequence 122, App
Sequence 124, App
Sequence 680, App
Sequence 4946, Ap
Sequence 164, App
Sequence 2, Appli
Sequence 28, Appli
Sequence 3188, Ap
Sequence 334, App
Sequence 20, Appl
Sequence 1068, App
Sequence 219, App
Sequence 1173, Ap
Sequence 121, App
Sequence 186, App
Sequence 45, Appl
Sequence 1812, Ap
Sequence 2238, Ap
Sequence 1321, Ap
Sequence 702, App
Sequence 362, App
Sequence 2692, Ap
Sequence 102, App
Sequence 7522, Ap
Sequence 4500, App
Sequence 726, App
Sequence 2646, Ap
Sequence 2868, Ap
Sequence 1936, Ap
Sequence 1660, Ap
Sequence 124, App
Sequence 998, App
Sequence 1760, Ap
Sequence 110, App
Sequence 3, Appli
Sequence 5888, Ap
Sequence 186, App
Sequence 4556, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 45, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 692, App
Sequence 1598, Ap
Sequence 1095, Ap
Sequence 1, Appli

99 26 44.8 13 6 US-10-511-559-645 Sequence 645, App
100 26 44.8 18 7 US-11-119-581-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-821-234-955
; Sequence 955, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 955
; LENGTH: 1187
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1187)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-955

Query Match 62.1%; Score 36; DB 6; Length 1187;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RLQQQLNLP 11
:|||||:
Db 220 RLQQQLNLPQ 229

RESULT 2
US-10-503-575-286
; Sequence 286, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: Koning, Frits
; APPLICANT: van Veelen, Petrus Antonius
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503.575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-286

Query Match 58.6%; Score 34; DB 6; Length 19;
Best Local Similarity 41.7%; Pred. No. 0.41;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRILQQINLPRI 12

Db 5 QQRIQQVNMPEYV 16
|:|:|:|:|:

RESULT 3
US-10-497-767-4
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVORKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VP1/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497.767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
US-10-497-767-4

Query Match 58.6%; Score 34; DB 6; Length 350;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRILQQINLP 10
:|||||:
Db 92 KRILQAVNFP 101

RESULT 4
US-11-082-389-386
; Sequence 386, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082.389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01